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SEQUENCE LISTING

<110> Rothschild, Max
Ciobanu, Dan
Malek, Massoud
Plastow, Graham

<120> Novel PRKAG3 Alleles and Use fo the Same as Genetic Markers for
Reprodcutive and Meat Quality Traits

<130> P04668US3

<150> 60/231045

<151> 2000-09-08

<150> 60/260,239

<151> 2001-01-08

<150> 60/299,111

<151> 2001-06-18

<160> 21

<170> PatentIn version 3.1

<210> 1

<211> 1873

<212> DNA

<213> Sus scrofa

<220>

<221> CDS

<222> (1)..(1392)

<223>

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gta	acc	acc	agc	tca	gaa	aga	agc	cat	ggg	gac	cag	ggg	aac	aag	gcc	96
Val	Thr	Thr	Ser	Ser	Glu	Arg	Ser	His	Gly	Asp	Gln	Gly	Asn	Lys	Ala	
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tct	aga	tgg	aca	agg	cag	gag	gat	gta	gag	gaa	ggg	ggg	cct	ccg	ggc	144
Ser	Arg	Trp	Thr	Arg	Gln	Glu	Asp	Val	Glu	Glu	Gly	Gly	Pro	Pro	Gly	
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ccg	agg	gaa	ggg	ccc	cag	tcc	agg	cca	gtt	gct	gag	tcc	acc	ggg	cag	192
Pro	Arg	Glu	Gly	Pro	Gln	Ser	Arg	Pro	Val	Ala	Glu	Ser	Thr	Gly	Gln	
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gag	gcc	aca	ttc	ccc	aag	gcc	aca	ccc	ttg	gcc	caa	gcc	gct	ccc	ttg	240
Glu	Ala	Thr	Phe	Pro	Lys	Ala	Thr	Pro	Leu	Ala	Gln	Ala	Ala	Pro	Leu	
65					70					75					80	

gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp 85 90 95	288
tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly 100 105 110	336
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val 115 120 125	384
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg 130 135 140	432
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met 145 150 155 160	480
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser 165 170 175	528
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aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val 210 215 220	672
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225 230 235 240	720
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tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro 275 280 285	864
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys 290 295 300	912
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac	960

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr	
305 310 315 320	
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg	1008
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val	
325 330 335	
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Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp	
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Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val	
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Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr	
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Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr	
385 390 395 400	
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Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly	
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gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc	1296
Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu	
420 425 430	
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Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile	
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Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala	
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gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt cccccctgct	1812
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
 35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
 50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
 65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
 85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
 100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
 115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
 130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
 145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
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Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
 180 185 190

Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys

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Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe		
245	250	255
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val		
260	265	270
Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro		
275	280	285
Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys		
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Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr		
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Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val		
325	330	335
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp		
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Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val		
355	360	365
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr		
370	375	380
Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr		
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Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly		
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Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu		
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Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
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<213> Sus scrofa

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Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Thr Lys Ala
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tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144
Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
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ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
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gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg 240
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
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Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
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tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc 336
Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg 384
Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg 432
Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

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cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser 165 170 175	528
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe 180 185 190	576
gcc ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys 195 200 205	624
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val 210 215 220	672
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225 230 235 240	720
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255	768
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 Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
 385 390 395 400
 ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg 1248
 Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
 405 410 415
 gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc 1296
 Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
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 gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc 1344
 Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
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<400> 4

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
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Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Thr Lys Ala
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190

Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
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 Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
 275 280 285
 Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
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 Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
 305 310 315 320
 Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
 325 330 335
 Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
 340 345 350
 Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
 355 360 365
 Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
 370 375 380
 Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
 385 390 395 400
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 Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
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<220>
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 Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
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 ccg agg gaa agt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192
 Pro Arg Glu Ser Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
 50 55 60
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 Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
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 gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac 288
 Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
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 Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
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 ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg 384
 Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
 115 120 125
 gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg 432
 Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
 130 135 140
 ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg 480
 Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
 145 150 155 160
 cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc 528
 His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
 165 170 175
 aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt 576
 Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
 180 185 190
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gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255			768
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 435 440 445

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 450 455 460

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 atctcagact ggggcaccct gaagatggga gtggccacgc ttatagctga gcagccttgt 1632
 gaaatctacc agcatcaaga ctactgtgg gaccactgct ttgtcccatt ctcagctgaa 1692
 atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtac 1752
 gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt cccccctgct 1812
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 g 1873

<210> 6
 <211> 464
 <212> PRT
 <213> Sus scrofa

<400> 6

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
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Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
 20 25 30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
 35 40 45

Pro Arg Glu Ser Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
 50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
 65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
 85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
 100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
 115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
 130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
 145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
 165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
 180 185 190

Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
 195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
 210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
 225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
 245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
 260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
 275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
 290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
 305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
 325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
 340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
 355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
 370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
 385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
 405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
 420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
 435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
 450 455 460

<210> 7
 <211> 1873
 <212> DNA
 <213> Sus scrofa

<220>
 <221> CDS
 <222> (1)..(1392)
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Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala		
1 5 10 15		
gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc		96
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala		
20 25 30		

tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly 35 40 45	144
ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln 50 55 60	192
gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu 65 70 75 80	240
gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp 85 90 95	288
tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly 100 105 110	336
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val 115 120 125	384
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg 130 135 140	432
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met 145 150 155 160	480
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser 165 170 175	528
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe 180 185 190	576
gcc ctg gtg gcc aac ggc atc cga gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Ile Arg Ala Ala Pro Leu Trp Asp Ser Lys 195 200 205	624
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val 210 215 220	672
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225 230 235 240	720
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255	768
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc	816

Lys	Pro	Leu	Val	Ser	Ile	Ser	Pro	Asn	Asp	Ser	Leu	Phe	Glu	Ala	Val		
			260					265					270				
tac	gcc	ctc	atc	aag	aac	cgg	atc	cac	cgc	ctg	ccg	gtc	ctg	gac	cct		864
Tyr	Ala	Leu	Ile	Lys	Asn	Arg	Ile	His	Arg	Leu	Pro	Val	Leu	Asp	Pro		
		275					280					285					
gtc	tcc	ggg	gct	gtg	ctc	cac	atc	ctc	aca	cat	aag	cgg	ctt	ctc	aag		912
Val	Ser	Gly	Ala	Val	Leu	His	Ile	Leu	Thr	His	Lys	Arg	Leu	Leu	Lys		
		290					295				300						
ttc	ctg	cac	atc	ttt	ggc	acc	ctg	ctg	ccc	cgg	ccc	tcc	ttc	ctc	tac		960
Phe	Leu	His	Ile	Phe	Gly	Thr	Leu	Leu	Pro	Arg	Pro	Ser	Phe	Leu	Tyr		
305					310				315						320		
cgc	acc	atc	caa	gat	ttg	ggc	atc	ggc	aca	ttc	cga	gac	ttg	gcc	gtg		1008
Arg	Thr	Ile	Gln	Asp	Leu	Gly	Ile	Gly	Thr	Phe	Arg	Asp	Leu	Ala	Val		
			325						330					335			
gtg	ctg	gaa	acg	gcg	ccc	atc	ctg	acc	gca	ctg	gac	atc	ttc	gtg	gac		1056
Val	Leu	Glu	Thr	Ala	Pro	Ile	Leu	Thr	Ala	Leu	Asp	Ile	Phe	Val	Asp		
			340					345					350				
cgg	cgt	gtg	tct	gcg	ctg	cct	gtg	gtc	aac	gaa	act	gga	cag	gta	gtg		1104
Arg	Arg	Val	Ser	Ala	Leu	Pro	Val	Val	Asn	Glu	Thr	Gly	Gln	Val	Val		
		355					360					365					
ggc	ctc	tac	tct	cgc	ttt	gat	gtg	atc	cac	ctg	gct	gcc	caa	caa	aca		1152
Gly	Leu	Tyr	Ser	Arg	Phe	Asp	Val	Ile	His	Leu	Ala	Ala	Gln	Gln	Thr		
	370					375					380						
tac	aac	cac	ctg	gac	atg	aat	gtg	gga	gaa	gcc	ctg	agg	cag	cgg	aca		1200
Tyr	Asn	His	Leu	Asp	Met	Asn	Val	Gly	Glu	Ala	Leu	Arg	Gln	Arg	Thr		
385					390					395					400		
ctg	tgt	ctg	gaa	ggc	gtc	ctt	tcc	tgc	cag	ccc	cac	gag	acc	ttg	ggg		1248
Leu	Cys	Leu	Glu	Gly	Val	Leu	Ser	Cys	Gln	Pro	His	Glu	Thr	Leu	Gly		
			405					410					415				
gaa	gtc	att	gac	cgg	att	gtc	cgg	gaa	cag	gtg	cac	cgc	ctg	gtg	ctc		1296
Glu	Val	Ile	Asp	Arg	Ile	Val	Arg	Glu	Gln	Val	His	Arg	Leu	Val	Leu		
			420					425				430					
gtg	gat	gag	acc	cag	cac	ctt	ctg	ggc	gtg	gtg	tcc	ctc	tct	gac	atc		1344
Val	Asp	Glu	Thr	Gln	His	Leu	Leu	Gly	Val	Val	Ser	Leu	Ser	Asp	Ile		
		435					440					445					
ctt	cag	gct	ctg	gtg	ctc	agc	cct	gct	gga	att	gat	gcc	ctc	ggg	gcc		1392
Leu	Gln	Ala	Leu	Val	Leu	Ser	Pro	Ala	Gly	Ile	Asp	Ala	Leu	Gly	Ala		
	450					455					460						
tgagaacctt	ggaacctttg	ctctcaggcc	acctggcaca	cctggaagcc	agtgaagggga												1452
gccgtggact	cagctctcac	ttcccctcag	ccccacttgc	tggtctggct	cttgttcagg												1512
taggctccgc	ccggggcccc	tggcctcagc	atcagcccct	cagtctccct	gggcacccag												1572

atctcagact ggggcaccct gaagatggga gtggcccagc ttatagctga gcagccttgt 1632
gaaatctacc agcatcaaga ctactgtgg gaccactgct ttgtcccatt ctgagctgaa 1692
atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtgac 1752
gtgccttcag gacctccggg gagttagagc tgcctctctc cagttcagtt cccccctgct 1812
gagaatgtcc ctggaaggaa gccagttaat aaaccttggt tggatggaat ttggagagtc 1872
g 1873

<210> 8
<211> 464
<212> PRT
<213> Sus scrofa

<400> 8

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
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Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
20 25 30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met

145		150		155		160
His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	165	170	175			
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	180	185	190			
Ala Leu Val Ala Asn Gly Ile Arg Ala Ala Pro Leu Trp Asp Ser Lys	195	200	205			
Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val	210	215	220			
Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	225	230	235			240
Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	245	250	255			
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val	260	265	270			
Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro	275	280	285			
Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys	290	295	300			
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr	305	310	315			320
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val	325	330	335			
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp	340	345	350			
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val	355	360	365			
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr	370	375	380			

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
 385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
 405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
 420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
 435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
 450 455 460

<210> 9
 <211> 1873
 <212> DNA
 <213> Sus scrofa

<220>
 <221> CDS
 <222> (1)..(1392)
 <223>

<400> 9
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 Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
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 gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96
 Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
 20 25 30
 tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144
 Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
 35 40 45
 ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192
 Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
 50 55 60
 gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg 240
 Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
 65 70 75 80
 gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac 288
 Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
 85 90 95

tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc	336
Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly	
100 105 110	
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg	384
Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val	
115 120 125	
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg	432
Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg	
130 135 140	
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg	480
Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met	
145 150 155 160	
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc	528
His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	
165 170 175	
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt	576
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	
180 185 190	
gcc ctg gtg gcc aac ggc gtc caa gcg gca cct ttg tgg gac agc aag	624
Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys	
195 200 205	
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg	672
Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val	
210 215 220	
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa	720
Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	
225 230 235 240	
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc	768
Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	
245 250 255	
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc	816
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val	
260 265 270	
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct	864
Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro	
275 280 285	
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag	912
Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys	
290 295 300	
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac	960
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr	
305 310 315 320	

cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val 325 330 335	1008
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp 340 345 350	1056
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val 355 360 365	1104
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr 370 375 380	1152
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr 385 390 395 400	1200
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly 405 410 415	1248
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu 420 425 430	1296
gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile 435 440 445	1344
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala 450 455 460	1392
tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaagcc agtgaaggga	1452
gccgtggact cagctctcac ttccctcag cccacttgc tggctctggct cttgttcagg	1512
taggctccgc cgggggcccc tggcctcagc atcagccct cagtctccct gggcacccag	1572
atctcagact ggggcaccct gaagatggga gtggcccagc ttatagctga gcagccttgt	1632
gaaatctacc agcatcaaga ctactgtgg gaccactgct ttgtccatt ctcagctgaa	1692
atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtgac	1752
gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt cccccctgct	1812
gagaatgtcc ctggaaggaa gccagttaat aaaccttggt tggatggaat ttggagagtc	1872
g	1873
<210> 10	
<211> 464	

<212> PRT
<213> Sus scrofa

<400> 10

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
1 5 10 15

Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
20 25 30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190

Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
 210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
 225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
 245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
 260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
 275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
 290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
 305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
 325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
 340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
 355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
 370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
 385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
 405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
 420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile

435

440

445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
 450 455 460

<210> 11
 <211> 1095
 <212> DNA
 <213> Sus scrofa

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 tcttcaggac cccaatctcc cccactccac tcgcctggct cttgtcttcc tctcctttgc 180
 cttctttgtt ccgctttgtt tcttcttctc cctctcctc cactcctcc ctctttcaaa 240
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 tagctgtgtg atttgtggca aattgcttca cctctctgag ctcaggtctc tcgttagtaa 360
 aacagggctg atagccatgc ccttcggata agattgccgt gagggttgaa tgagaaattt 420
 gttggaggac aagccctttg aagcttccca atattaaata tttttattta tttatttatt 480
 ttttgtcttt ttgctattcc tttgggcccgc tcccacggca tatggagggt cccaggctag 540
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 gccgcatctg caacctacac cacagctcac ggcaacgccg gatcgtaaac ccaactgagca 660
 ggggcaggca ccgaacctgc aacctcatgg ttcctagtgg gattcgtaaa ccaactgcgcc 720
 acgacgggaa ctcccgaata ttaaatatta ttattagtaa cattttaatg gaatttattg 780
 tgttactccc cattaaccaa acaggtccca ttctcccttg cagagatgag cttcctagag 840
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